

GenCore version 5.1.6
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OM nucleic - nucleic search, using BW model

Run on: July 23, 2005, 22:27:07 ; Search time 1690 Seconds
(without alignments)
458.748 Million cell updates/sec

Title: us-09-973-945b-9

Perfect score: 16

Sequence: 1 gaatacatatatttc 16

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:1:
1: gb_ba:*
2: gb_hgt:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	103	9 HS46A3F	255508 H.sapiens C
2	16	100.0	103	9 HS46A3F	255508 H.sapiens C
3	16	100.0	280	6 CQ709049	CQ709049 Sequence
4	16	100.0	280	6 CQ709049	CQ709049 Sequence
5	16	100.0	558	11 G81093	G81093 S208P6414RC
6	16	100.0	558	11 G81093	G81093 S208P6414RC
7	16	100.0	559	11 AB165691	AB165691 Bos tauru
8	16	100.0	559	11 AB165691	AB165691 Bos tauru
9	16	100.0	566	11 BV070170	BV070170 S208P6211
10	16	100.0	566	11 BV070170	BV070170 S208P6211
11	16	100.0	653	8 IMA295790	AJ295790 Isoplepis
12	16	100.0	653	8 IMA295790	AJ295790 Isoplepis
13	16	100.0	1022	8 AF518122	AF518122 Templeton
14	16	100.0	1022	8 AF518122	AF518122 Templeton
15	16	100.0	1413	5 BC068189	BC068189 Danio rer
16	16	100.0	1413	5 BC068189	BC068189 Danio rer
17	16	100.0	4381	9 HSM807863	BX647717 Homo sapi
18	16	100.0	4381	9 HSM807863	BX647717 Homo sapi
19	16	100.0	5728	6 AX345003	AX345003 Sequence

C 20	16	100.0	5728	6	AX345003	AX345003 Sequence
C 21	16	100.0	6059	9	AB023158	AB023158 Homo sapi
C 22	16	100.0	6059	9	AB023158	AB023158 Homo sapi
C 23	16	100.0	6059	9	AY037299	AY037299 Homo sapi
C 24	16	100.0	6059	9	AY037299	AY037299 Homo sapi
C 25	16	100.0	6992	6	CO593660	CO593660 Sequence
C 26	16	100.0	6992	6	CO593660	CO593660 Sequence
C 27	16	100.0	7733	3	DROAGPDD	D50090 Drosophila
C 28	16	100.0	7733	3	DROAGPDD	D50090 Drosophila
C 29	16	100.0	7823	6	AX278034	AX278034 Sequence
C 30	16	100.0	7823	6	AX278034	AX278034 Sequence
C 31	16	100.0	7823	6	AX323803	AX323803 Sequence
C 32	16	100.0	7823	6	AX323803	AX323803 Sequence
C 33	16	100.0	7823	6	AX344488	AX344488 Sequence
C 34	16	100.0	7823	6	AX344488	AX344488 Sequence
C 35	16	100.0	7823	6	AX346962	AX346962 Sequence
C 36	16	100.0	7823	6	AX346962	AX346962 Sequence
C 37	16	100.0	8617	3	DMU19731	U19731 Drosophila
C 38	16	100.0	8617	3	DMU19731	U19731 Drosophila
C 39	16	100.0	23501	9	AC126176	AC126176 Homo sapi
C 40	16	100.0	23501	9	AC126176	AC126176 Homo sapi
C 41	16	100.0	23579	6	AX647373	AX647373 Sequence
C 42	16	100.0	23579	6	AX647373	AX647373 Sequence
C 43	16	100.0	26246	3	CET12G3	Z68752 Caenorhabdi
C 44	16	100.0	26246	3	CET12G3	Z68752 Caenorhabdi
C 45	16	100.0	28833	9	AC096581	AC096581 Homo sapi

ALIGNMENTS

RESULT 1
HS46A3F
LOCUS
DEFINITION
H.sapiens Cpg island DNA genomic MseI fragment, clone 46a3, forward
read cpg46a3.ftla.
255508
ACCESSION
255508.1 GI:1021549
VERSION
Cpg island; genomic MseI fragment.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM

REFERENCE
1
Gross, S.H., Charlton, J.A., Nan, X. and Bird, A.P.
Purification of Cpg islands using a methylated DNA binding column
Nat. Genet. 6 (3), 226-244 (1994)
94282070
MEDLINE
PUBMED
8012384

REFERENCE
2 (bases 1 to 103)
Macdonald, M., Huckle, E., Wilkinson, P. and Mickle, G.
Direct Submision
Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgehire,
CB10 1RQ, England. E-mail contact: humquerry@sanger.ac.uk

COMMENT
Clones are available from the UK MRC Human Genome Mapping Project
Resource Centre, Hinxton, Cambridgehire CB10 1RQ, UK. See URL:
http://www.hgmp.mrc.ac.uk/ for details
or contact: biohelp@hgmp.mrc.ac.uk.

FEATURES
source
1..103
location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="46a3"
/sex="male"
/tissue_type="blood"
/clone_lib="CGI-1"
/dev_stage="adult"

ORIGIN

Query Match 100.0%; Score 16; DB 9; Length 103;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;

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OM nucleic - nucleic search, using sw model

Run on: July 23, 2005, 22:24:32 ; Search time 272 Seconds
(without alignments)
348.220 Million cell updates/sec

Title: US-09-973-945B-9
Perfect score: 16
Sequence: 1 gaatatatataatc 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneeqn1980s:*
2: geneeqn1990s:*
3: geneeqn2000s:*
4: geneeqn2001s:*
5: geneeqn2001bs:*
6: geneeqn2002as:*
7: geneeqn2002bs:*
8: geneeqn2003as:*
9: geneeqn2003bs:*
10: geneeqn2003cs:*
11: geneeqn2003ds:*
12: geneeqn2004as:*
13: geneeqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	16	100.0	16	6	ABN87616	Abn87616 Native in
2	16	100.0	16	6	ABN87616	Abn87616 Native in
3	16	100.0	16	6	ABN87617	Abn87617 Native in
4	16	100.0	16	6	ABN87617	Abn87617 Native in
5	16	100.0	29	6	ABN87619	Abn87619 Native in
6	16	100.0	29	6	ABN87619	Abn87619 Native in
7	16	100.0	29	6	ABN87618	Abn87618 Native in
8	16	100.0	29	6	ABN87618	Abn87618 Native in
9	16	100.0	46	6	ABN87612	Abn87612 Arabidops
10	16	100.0	46	6	ABN87612	Abn87612 Arabidops
11	16	100.0	48	6	ABN87612	Abn87612 Arabidops
12	16	100.0	48	6	ABN87612	Abn87612 Arabidops
13	16	100.0	58	6	ABN87608	Abn87608 Arabidops
14	16	100.0	58	6	ABN87608	Abn87608 Arabidops
15	16	100.0	336	4	AAK77535	Aak77535 Human imm
16	16	100.0	336	4	AAK77535	Aak77535 Human imm
17	16	100.0	757	4	AAK78539	Aak78539 Human imm
18	16	100.0	757	4	AAK78539	Aak78539 Human imm
19	16	100.0	757	4	AAK78540	Aak78540 Human imm
20	16	100.0	757	4	AAK78540	Aak78540 Human imm

21	16	100.0	5728	6	ABL32101	ABL32101 Human imm
22	16	100.0	5728	6	ABL32101	ABL32101 Human imm
23	16	100.0	6992	4	ABL16118	ABL16118 Drosophi
24	16	100.0	6992	4	ABL16118	ABL16118 Drosophi
25	16	100.0	7823	4	AA545489	Aa545489 Chemicall
26	16	100.0	7823	4	AA545489	Aa545489 Chemicall
27	16	100.0	7823	6	ABL34060	ABL34060 Human imm
28	16	100.0	7823	6	ABL34060	ABL34060 Human imm
29	16	100.0	7823	6	ABL34060	ABL34060 Human imm
30	16	100.0	7823	6	ABL34060	ABL34060 Human imm
31	16	100.0	7823	6	ABL34060	ABL34060 Human imm
32	16	100.0	7823	6	ABL34060	ABL34060 Human imm
33	16	100.0	7823	6	ABL34060	ABL34060 Human imm
34	16	100.0	23579	10	AD087112	Adc87112 Human GPC
35	16	100.0	23579	10	AD087112	Adc87112 Human GPC
36	16	100.0	48133	11	ACN44860	Acn44860 Mouse gen
37	16	100.0	48133	11	ACN44860	Acn44860 Mouse gen
38	16	100.0	62705	12	AD009371	Adg09371 Human Ang
39	16	100.0	62705	12	AD009371	Adg09371 Human Ang
40	16	100.0	106286	6	AB555320_4	Continuation (5 of
41	16	100.0	106286	6	AB555320_4	Continuation (5 of
42	16	100.0	110000	6	AB555320_2	Continuation (3 of
43	16	100.0	110000	12	AD059398_2	Continuation (3 of
44	16	100.0	110000	12	AD059398_2	Continuation (3 of
45	16	100.0	110000	13	ABD32911_6	Continuation (7 of

ALIGNMENTS

RESULT 1
ABN87616 standard; DNA; 16 BP.
ID ABN87616
AC ABN87616
XX
DT 07-AUG-2002 (first entry)
XX
XX Native insulator probe N116 SEQ ID NO:9.
DE
XX Arabidopsis thaliana; genetic insulator; gene promoter; plant;
KW transgenic plant; probe; ss.
XX
OS Arabidopsis thaliana.
XX
PN MO200234035-A1.
XX
PD 02-MAY-2002.
XX
XX 11-OCT-2001; 2001WO-US031712.
XX PF
XX 20-OCT-2000; 2000US-0241735P.
XX PR
XX (KENT) UNIV KENTUCKY RES FOUND.
XX
XX Gan S, Xie M;
XX
XX WPI; 2002-471421/50.
XX
XX New isolated or recombinant polynucleotide cloned from Arabidopsis
PT thaliana, useful for minimizing or eliminating the position effect on a
PT transgene in a plant.
XX
XX Claim 1; Page 21; 45pp; English.
XX
XX The present invention describes an isolated or a recombinant
XX polynucleotide (I) comprising at least one copy of a polynucleotide
XX having the sequence GAAATATATATATTC (S1) of 16 nucleotides, or a
XX polynucleotide which is a variant or fragment of S1, where the variant or
XX fragment has a plant genetic insulator activity. Also described are
XX methods: (1) (M1) expressing a polypeptide in a plant cell, involving
XX providing a vector comprising (I), a structural polynucleotide coding for
XX a polypeptide, inserting the vector into a plant cell, where the genetic

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OM nucleic - nucleic search, using sw model

Run on: July 23, 2005, 22:32:33 ; Search time 402 Seconds
(without alignments)
252,508 Million cell updates/sec

Title: US-09-973-945B-9

Perfect score: 16

Sequence: 1 gaatatatattatc 16

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7173243 seqs, 3172129809 residues

Total number of hits satisfying chosen parameters: 14346486

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:
22: /cgn2_6/ptodata/2/pubpna/US10J_PUBCOMB.seq:
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:
24: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:
25: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:
26: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	16	9	US-09-973-945A-9
2	16	100.0	16	9	US-09-973-945A-9
3	16	100.0	16	9	US-09-973-945A-10
4	16	100.0	16	9	US-09-973-945A-10
5	16	100.0	29	9	US-09-973-945A-11
6	16	100.0	29	9	US-09-973-945A-11
7	16	100.0	29	9	US-09-973-945A-12

C	8	16	100.0	29	9	US-09-973-945A-12	Sequence 12, Appl
C	9	16	100.0	46	9	US-09-973-945A-5	Sequence 5, Appl
C	10	16	100.0	46	9	US-09-973-945A-5	Sequence 5, Appl
C	11	16	100.0	58	9	US-09-973-945A-1	Sequence 1, Appl
C	12	16	100.0	58	9	US-09-973-945A-1	Sequence 1, Appl
C	13	16	100.0	277	20	US-10-425-115-72551	Sequence 72551, A
C	14	16	100.0	277	20	US-10-425-115-72551	Sequence 72551, A
C	15	16	100.0	280	17	US-10-242-535A-53975	Sequence 53975, A
C	16	100.0	280	17	US-10-242-535A-53975	Sequence 53975, A	
C	17	16	100.0	280	18	US-10-085-783A-53975	Sequence 53975, A
C	18	16	100.0	280	18	US-10-085-783A-53975	Sequence 53975, A
C	19	16	100.0	288	19	US-10-674-124A-25880	Sequence 25880, A
C	20	16	100.0	288	19	US-10-674-124A-25880	Sequence 25880, A
C	21	16	100.0	488	13	US-10-027-632-319280	Sequence 319280, A
C	22	16	100.0	488	13	US-10-027-632-319280	Sequence 319280, A
C	23	16	100.0	488	17	US-10-027-632-319280	Sequence 319280, A
C	24	16	100.0	488	17	US-10-027-632-319280	Sequence 319280, A
C	25	16	100.0	572	13	US-10-027-632-319280	Sequence 319280, A
C	26	16	100.0	572	13	US-10-027-632-319280	Sequence 319280, A
C	27	16	100.0	572	17	US-10-027-632-319280	Sequence 319280, A
C	28	16	100.0	572	17	US-10-027-632-319280	Sequence 319280, A
C	29	16	100.0	771	13	US-10-027-632-145013	Sequence 145013, A
C	30	16	100.0	771	13	US-10-027-632-145013	Sequence 145013, A
C	31	16	100.0	771	13	US-10-027-632-145013	Sequence 145013, A
C	32	16	100.0	771	13	US-10-027-632-145013	Sequence 145013, A
C	33	16	100.0	771	17	US-10-027-632-145013	Sequence 145013, A
C	34	16	100.0	771	17	US-10-027-632-145013	Sequence 145013, A
C	35	16	100.0	771	17	US-10-027-632-145013	Sequence 145013, A
C	36	16	100.0	771	17	US-10-027-632-145013	Sequence 145013, A
C	37	16	100.0	5728	15	US-10-311-455-74	Sequence 74, Appl
C	38	16	100.0	5728	15	US-10-311-455-74	Sequence 74, Appl
C	39	16	100.0	7823	14	US-10-239-676-197	Sequence 197, App
C	40	16	100.0	7823	14	US-10-239-676-197	Sequence 197, App
C	41	16	100.0	7823	15	US-10-311-455-2033	Sequence 2033, Ap
C	42	16	100.0	7823	15	US-10-311-455-2033	Sequence 2033, Ap
C	43	16	100.0	7823	15	US-10-240-453-291	Sequence 291, App
C	44	16	100.0	7823	15	US-10-240-453-291	Sequence 291, App
C	45	16	100.0	23579	15	US-10-017-161-1909	Sequence 1909, Ap

ALIGNMENTS

RESULT 1
US-09-973-945A-9
Sequence 9, Application US/09973945A
Patent No. US20020169297A1
GENERAL INFORMATION:
APPLICANT: University of Kentucky Research Foundation
APPLICANT: GEN, Susheng
TITLE OF INVENTION: Genetic Insulator for Preventing Influence By Another Gene
FILE REFERENCE: 050229-0287
CURRENT APPLICATION NUMBER: US/09/973, 945A
PRIOR FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 60/241, 735
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 16
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-973-945A-9

Query Match 100.0%; Score 16; DB 9; Length 16;
Beet Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GAATATATATATATTC 16
1 GAATATATATATATTC 16

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OM nucleic - nucleic search, using bw model

Run on: July 23, 2005, 22:27:43 ; Search time 1838 Seconds
(without alignments)
331.354 Million cell updates/sec

Title: US-09-973-945B-9

Perfect score: 16
Sequence: 1 Gattatattatattc 16

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	113	5	BQ173432 Bg_PSGR_0
2	16	100.0	113	5	BQ173432 Bg_PSGR_0
3	16	100.0	157	7	CN649902 Bg_PSGRS
4	16	100.0	157	7	CN649902 Bg_PSGRS
5	16	100.0	188	5	BU035358 CHU6M16.Y
6	16	100.0	188	5	BU035358 CHU6M16.Y
7	16	100.0	202	6	CF011114 OBU6C03.P
8	16	100.0	202	6	CF011114 OBU6C03.P
9	16	100.0	230	8	AO927963 RPCI-23-2
10	16	100.0	230	8	AO927963 RPCI-23-2
11	16	100.0	245	7	CN650739 Bg_PSGRS
12	16	100.0	245	7	CN650739 Bg_PSGRS
13	16	100.0	269	2	BF655072 Bg_PSGRS
14	16	100.0	269	2	BF655072 Bg_PSGRS
15	16	100.0	292	5	BX713976 BX713976
16	16	100.0	292	5	BX713976 BX713976
17	16	100.0	303	7	CN650230 Bg_PSGRS
18	16	100.0	303	7	CN650230 Bg_PSGRS
19	16	100.0	303	7	CN652060 Bg_PSGRS
20	16	100.0	303	7	CN652060 Bg_PSGRS
21	16	100.0	312	8	AO481031 RPCI-11-2
22	16	100.0	312	8	AO481031 RPCI-11-2
23	16	100.0	320	4	BI244201 Bg_PSGR_0
24	16	100.0	320	4	BI244201 Bg_PSGR_0

25	16	100.0	330	5	BP716094
26	16	100.0	330	5	BP716094
27	16	100.0	338	9	TA231B03P
28	16	100.0	338	9	TA231B03P
29	16	100.0	352	8	BZ679256 PUBGH19TD
30	16	100.0	352	8	BZ679256 PUBGH19TD
31	16	100.0	352	8	BZ686943 PUBGH19TD
32	16	100.0	352	8	BZ686943 PUBGH19TD
33	16	100.0	365	7	CN649868 Bg_PSGRS
34	16	100.0	365	7	CN649868 Bg_PSGRS
35	16	100.0	374	4	BI404261 M1-P-CP1-
36	16	100.0	374	4	BI404261 M1-P-CP1-
37	16	100.0	379	5	BP679193 BP679193
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ALIGNMENTS

RESULT 1
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DEFINITION BQ173432 113 bp mRNA linear EST 18-SRP-2002
BQ173432
BQ173432.2 GI:23188133
BQ173432
Bg_PSGR_03G05.T7 Echinococcus granulosis protoscolex (full length
enriched) Echinococcus granulosis cDNA clone Bg_PSGR_03G05.5, mRNA
sequence.

ACCESSION BQ173432
VERSION BQ173432
KEYWORDS EST
SOURCE Echinococcus granulosis
ORGANISM Echinococcus granulosis
Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
Cyclophyllidae; Taeniidae; Echinococcus.

REFERENCE 1 (bases 1 to 113)
Fernandez, C. and Maizels, R.M.
A survey of genes expressed in Echinococcus granulosis metacystode
Unpublished (2001)
On Apr 29, 2002 this sequence version replaced gi:20337834.
COMMENT
Contact: Maizels RM
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, West Mains Road, Edinburgh EH93JT, Scotland
Tel: +44 131 650 5511
Fax: +44 131 650 5450
Email: r.maizels@ed.ac.uk
The library was created by Dr Cecilia Fernandez in conjunction with
Prof. R. Maizels. Sequencing was also performed by Cecilia. The
sequence contained a Polya tail (trimmed)
PCR Primers
FORWARD: M13P
BACKWARD: M13R
Plate: 03 row: G column: 05
Seq primer: 77
High quality sequence stop: 113.
Location/Qualifiers
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/clone="Bg_PSGR_03G05"
/dev_stage="larva (protoscolex)"
/clone_id="Echinococcus granulosis protoscolex (full
length enriched)"
/note="Vector: pSPORT1; Site 1: SalI (5' end); Site 2: NotI
(3' end); Echinococcus granulosis is a cestode parasite of
dogs (definitive host) and various domestic and wild
animals as well as humans (intermediate hosts). The

FEATURES

source

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2005, 22:28:38 ; Search time 99 Seconds
(without all constraints)

264.449 Million cell updates/sec

Title: US-09-973-945B-9

Sequence: 1 gaatatatatatc 16

Scoring table: IDENTITY_NUC

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA:*

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4: /cgn2_6/prodata/1/ina/6B_COMB_seg.*
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6: /cgn2_6/prodata/1/ina/backfiles1_seg.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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1	16	100.0	48	3	US-09-545-244A-8	Sequence 8, Appl1
2	16	100.0	48	3	US-09-545-244A-8	Sequence 8, Appl1
3	16	100.0	37966	4	US-09-949-016-12566	Sequence 12566, Appl1
4	16	100.0	37966	4	US-09-949-016-12566	Sequence 12566, Appl1
5	16	100.0	92581	4	US-09-949-016-12162	Sequence 12162, Appl1
6	16	100.0	92581	4	US-09-949-016-12162	Sequence 12162, Appl1
7	16	100.0	92581	4	US-09-949-016-16542	Sequence 16542, Appl1
8	16	100.0	92581	4	US-09-949-016-16542	Sequence 16542, Appl1
9	16	100.0	92581	4	US-09-949-016-16542	Sequence 16542, Appl1
10	16	100.0	251672	4	US-09-949-016-17286	Sequence 17286, Appl1
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12	16	100.0	301828	4	US-09-949-016-13969	Sequence 13969, Appl1
13	16	100.0	301828	4	US-09-949-016-13969	Sequence 13969, Appl1
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16	15.6	97.5	1974	1	US-08-413-135-3	Sequence 3, Appl1
17	15.6	97.5	1974	1	US-08-971-395-3	Sequence 3, Appl1
18	15.6	97.5	1974	1	US-08-971-395-3	Sequence 3, Appl1
19	15	93.8	236	4	US-09-270-767-7457	Sequence 7457, Appl1
20	15	93.8	236	4	US-09-270-767-7457	Sequence 7457, Appl1
21	15	93.8	236	4	US-09-270-767-7457	Sequence 7457, Appl1
22	15	93.8	236	4	US-09-270-767-7457	Sequence 7457, Appl1
23	15	93.8	271	1	US-07-906-871-1	Sequence 1, Appl1
24	15	93.8	271	1	US-07-906-871-1	Sequence 1, Appl1
25	15	93.8	427	4	US-09-854-133-551	Sequence 551, Appl1
26	15	93.8	427	4	US-09-854-133-551	Sequence 551, Appl1
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C	28	15	93.8	488	4	US-09-270-767-5493	Sequence 20775, A
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C	30	15	93.8	488	4	US-09-270-767-20775	Sequence 20775, A
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C	32	15	93.8	570	4	US-09-949-016-130195	Sequence 130195, A
C	33	15	93.8	600	4	US-09-270-767-10320	Sequence 10320, A
C	34	15	93.8	600	4	US-09-270-767-10320	Sequence 10320, A
C	35	15	93.8	601	4	US-09-949-016-61005	Sequence 61005, A
C	36	15	93.8	601	4	US-09-949-016-61005	Sequence 61005, A
C	37	15	93.8	601	4	US-09-949-016-135263	Sequence 135263, A
C	38	15	93.8	601	4	US-09-949-016-135263	Sequence 135263, A
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C	41	15	93.8	601	4	US-09-949-016-153592	Sequence 153592, A
C	42	15	93.8	601	4	US-09-949-016-153592	Sequence 153592, A
C	43	15	93.8	836	4	US-09-270-767-28507	Sequence 28507, A
C	44	15	93.8	836	4	US-09-270-767-28507	Sequence 28507, A
C	45	15	93.8	1826	4	US-09-023-655-1297	Sequence 1297, A

ALIGNMENTS

RESULT 1
US-09-545-244A-8
Sequence 8, Application US/09545244A

GENERAL INFORMATION:

APPLICANT: Xie, Mingtang

10 TITLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto
11
12 FID NUMBER: 050000 0010

CURRENT APPLICATION NUMBER: US/09/545,244A

NUMBER OF SEQ ID NOS: 12

; SEQ ID NO 8

TYPE: DNA

US-09-545-244A-8

Query Match	Score 16;	DB 3;	Length 48;
100.0%			

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

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Db	9	GAATATATATATATTC	2

RESULT 2
US-09-545-244A-8/C

Patent No. 6388170

APPLICANT: Gan, Sue

APPLICANT: He, Yuehui

FILE REFERENCE: 050229-0210

CURRENT FILING DATE: 2000-04-07

; SOFTWARE: PatentIn version 3.1

LENGTH: 48

ORGANISM: synthetic construct

Query Match 100.0%; Score 16; DB 3; Length 48;